Additional File 8. Identity of Dact proteins and most conserved regions.

Amino acid identity of Dact proteins based on (A) the full, gapped alignment, (B) the trimmed alignment used for the phylogenetic trees, (C) the alignment for the exon1-3 encoded motif 2 that encompasses the leucine zipper, a nuclear export signal and that participates in Alk5 inhibition, and (D) the C-terminal motif 11 encoded by exon 4 that encompasses a predicted nuclear localization signal, the Vangl binding domain and the PDZ binding domain. Only sequences that were complete (A, B) or for which the respective motif sequence was available (C,D) were used.

(A) whole sequence

	Dact1	**Dact3**	**Dact2**	**Dact4**	**Lj/Pm**	**Bfl**
Dact1	56.0%	18.7%	19.5%	10.3%	15.4%	8.8%
Dact3	18.7%	26.3%	13.2%	7.4%	11.3%	6.7%
Dact2	19.5%	13.2%	40.6%	11.4%	14.0%	8.4%
Dact4	10.3%	7.4%	11.4%	16.2%	7.7%	5.3%
Lj/Pm	15.4%	11.3%	14.0%	7.7%	11.3%	6.5%
Bfl	8.8%	6.7%	8.4%	5.3%	6.5%	ID

Overall protein ID: 18.5%

(B) whole sequence trimmed

	Dact1	**Dact3**	**Dact2**	**Dact4**	**Lj/Pm**	**Bfl**
Dact1	81.5%	44.4%	48.1%	28.9%	42.0%	25.4%
Dact3	44.4%	47.8%	33.6%	19.5%	30.6%	19.5%
Dact2	48.1%	33.6%	66.8%	32.4%	37.5%	24.3%
Dact4	28.9%	19.5%	32.4%	47.4%	23.5%	17.6%
Lj/Pm	42.0%	30.6%	37.5%	23.5%	35.0%	18.5%
Bfl	24.5%	19.5%	24.3%	17.6%	18.5%	ID

trimmed: 40.4%

(C) motif 2 (encoded by exons 1-3)

	Dact1	**Dact3**	**Dact2**	**Dact4**	**Lj/Pm**	**Bfl**
Dact1	90.4%	27.2%	61.4%	29.0%	46.5%	29.8%
Dact3*	27.2%	27.7%	27.1%	15.0%	22.3%	18.4%
Dact2	61.4%	27.1%	85.1%	31.4%	46.4%	27.8%
Dact4	29.0%	15.0%	31.4%	37.1%	27.3%	17.3%
Lj/Pm	46.5%	22.3%	46.4%	27.3%	37.6%	20.8%
Bfl	29.8%	18.4%	27.8%	17.3%	20.8%	ID

(D) motif 11 (C-terminus)

	Dact1	**Dact3**	**Dact2**	**Dact4**	**Lj/Pm**	**Bfl**
Dact1	81.8%	43.6%	42.5%	12.9%	27.4%	15.4%
Dact3	43.6%	54.7%	31.8%	11.3%	22.4%	13.3%
Dact2	42.5%	31.8%	61.2%	15.3%	23.8%	12.5%
Dact4	12.3%	11.3%	15.3%	33.0%	9.1%	8.3%
Lj/Pm	27.4%	22.4%	23.8%	9.1%	19.2%	8.6%
Bfl	15.4%	13.3%	12.5%	8.3%	8.6%	ID

* strong reduction of motif 2 in teleost dact3b
ID = identical